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Serial No. Not Yet Known  
Filed: Herewith

Page 2 [Preliminary Amendment Accompanying Reques Under 37 C.F.R. §1.160  
For Divisional Application - November 12, 1999]

**AMEND THIS APPLICATION AS FOLLOWS**

**In The Specification**

Page 1, line 1, before "BACKGROUND OF THE INVENTION" insert the following:

-- CROSS-REFERENCE TO OTHER RELATED APPLICATIONS

This application is a divisional of U.S. Patent Application  
Serial No. 09/104,067 filed on June 24, 1998. --

**In The Title:**

Change the title of the invention to:

-- NOVEL SPECIFIC TARGET NUCLEIC ACID DETECTION AND  
AMPLIFICATION PROCESSES, AND COMPOSITIONS USEFUL FOR  
PRODUCING ONE OR MORE COPIES OF SPECIFIC TARGET NUCLEIC  
ACID SEQUENCES -- .

**In The Claims**

✓  
Cancel claim 1.

Add new claims 60-145 as follows:

-- 60. (NEW) A process for detecting the presence of a specific target nucleic acid sequence comprising the steps of:

1) providing one or more first initial primers or first nucleic acid constructs comprising two segments:

(A) a first segment (i) being substantially complementary to a portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said first initial primers or first nucleic acid constructs with said specific target nucleic acid sequence as a template and where in the absence of a denaturation step, the first initial primers or first nucleic acid constructs being capable of participation in the formation of a stem-loop structure after said specific target nucleic acid sequence is used as a template for extension;

2) mixing said first initial primers or nucleic acid constructs with substrates, buffer, a template-dependent polymerizing enzyme and a sample to be tested for the presence of said specific target nucleic acid;

3) incubating said mixture under temperature conditions sufficient for binding of said first initial primers or first nucleic acid constructs to said specific target nucleic acid sequence, extension of said first initial primers or first nucleic acid constructs and formation of stem-loop structures; and

4) detecting the presence of said stem-loop structure formed by self-annealing between the second segment of said first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of said first initial primer or first nucleic acid construct, thereby detecting the presence of said specific target nucleic acid sequence or its complement. --

-- 61. (NEW) The process of claim 60, wherein said template polymerizing enzyme comprises a member selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, DNA ligase and a combination of any of the foregoing. --

-- 67. (NEW) The process of claim 60, wherein said providing step 1) at least one second initial primer or second nucleic acid construct is provided, wherein said second initial primer or second nucleic acid construct comprises a first segment substantially complementary to sequences that are synthesized after extension of said first initial primer or first nucleic acid construct. --

-- 68. (NEW) The process of claim 67, wherein said second initial primer or second nucleic acid construct further comprises a second segment being (i) substantially non-identical to the first segment of said second initial primer or second nucleic acid construct; (ii) substantially identical to a portion of said extended first initial primer or first nucleic acid construct; and (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said second initial primer or second nucleic acid construct with said extended first initial primer or nucleic acid construct as a template. --

-- 69. (NEW) The process of claim 67, wherein said second initial primers, extended initial primers, nucleic acid constructs or extended nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 70. (NEW) The process of claims 67 or 68, wherein said second initial primer or second nucleic acid construct or said extended second initial primer or extended second nucleic acid construct comprises one or more modified nucleotides having detectable labels. --

-- 71. (NEW) The process of claims 69 or 70, wherein said detectable labels are selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 72. (NEW) The process of any of claims 60, 61, 62, 63, 64, 65, 66, 67, 68, 70 or 71, wherein the detection of the formation of a stem-loop structure takes place after nucleic acid synthesis is substantially completed. --

-- 73. (NEW) The process of any of claims 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or 71, wherein the detection of the formation of a stem-loop structure takes place before nucleic acid synthesis is substantially completed. --

-- 74. (NEW) A process for amplifying a specific target nucleic acid sequence comprising the steps of:

providing:

- (i) said specific target nucleic acid sequence;
- (ii) one or more first initial primers or first nucleic acid constructs comprising two segments:

(A) a first segment (i) being substantially complementary to a portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of the first initial primer or first nucleic acid construct with said specific target nucleic acid sequence as a template and wherein the portion of said specific target nucleic acid that comprises sequences complementary to the first segment of the first initial primer or first nucleic acid construct and the portion of said specific target nucleic acid that comprises sequences substantially identical to the second segment of the first initial primer or first nucleic acid construct are in close proximity to each other; and

- (iii) substrates, buffer and a template-dependent polymerizing enzyme; and

incubating said specific target nucleic acid sequence and said first initial primer or first nucleic acid construct in the presence of said substrates, buffer and template-dependent polymerizing enzyme under appropriate temperature conditions, thereby producing one or more copies of said specific target nucleic acid sequence or its complement. --

-- 75. (NEW) The process of claim 74, wherein said providing step, at least one second initial primer or second nucleic acid construct is provided, wherein said second initial primer or second nucleic acid construct comprises a first segment substantially complementary to sequences that are synthesized after extension of said first initial primer or first nucleic acid construct. --

-- 76. (NEW) The process of claim 75, wherein said second initial primer or nucleic acid construct further comprises a second segment being (i) substantially non-identical to the first segment of said second initial primer or nucleic acid construct; (ii) substantially identical to a portion of said extended first initial primer or first nucleic acid construct; and (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said second initial primer or second nucleic acid construct with said extended first initial primer or extended first nucleic acid construct as a template. --

-- 77. (NEW) The process of claims 74, 75 or 76, wherein the synthesis of one or more copies of sequences derived from the specific target nucleic acid sequence or its complement is carried out under isothermal conditions. --

-- 78. (NEW) The process of claim 74, 75 or 76, wherein the synthesis of one or more copies of sequences derived from the specific target nucleic acid sequence or its complement is carried out with one or more limited cycle or full cycle steps. --

-- 79. (NEW) The process of any of claims 74, 75, 76, 77 or 78, wherein less than about 50 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 80. (NEW) The process of claim 79, wherein less than about 10 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 81. (NEW) The process of claim 80, wherein the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct is adjacent to the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 82. (NEW) The process of claim 74, wherein said first initial primers, extended first initial primers, first nucleic acid constructs or extended first nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 83. (NEW) The process of claim 74, wherein said first initial primer or first nucleic acid construct or said extended first initial primer or first nucleic acid construct comprises one or more modified nucleotides having detectable labels. --

-- 84. (NEW) The process of claims 82 or 83, wherein said detectable labels are selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 85. (NEW) The process of claim 74, wherein said template polymerizing enzyme comprises a member selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, DNA ligase and a combination of any of the foregoing. --

-- 86. (NEW) A process for detecting the presence of a specific target nucleic acid sequence comprising the steps of:

1) providing one or more first initial primers or first nucleic acid constructs comprising two segments:

(A) a first segment (i) being substantially complementary to a portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension, and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of the first initial primer or first nucleic acid construct with said specific target nucleic acid sequence as a template and wherein the portion of said specific target nucleic acid that comprises sequences complementary to the first segment of the first initial primer or nucleic acid construct and the portion of said target nucleic acid that comprises sequences substantially identical to the second segment of said first initial primer or first nucleic acid construct are in close proximity to each other;

2) mixing said first initial primer or first nucleic acid construct with substrates, buffer, a template-dependent polymerizing enzyme and a sample to be tested for the presence of said specific target nucleic acid;

3) incubating said mixture under temperature conditions sufficient for binding of said first initial primers or first nucleic acid constructs to said specific target nucleic acid, extension of said first initial primers or first nucleic acid constructs and formation of stem-loop structures; and

4) detecting the presence of said stem-loop structure formed by self-annealing between the second segment of said first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of said first initial primer or first nucleic acid construct, thereby detecting the presence of said specific target nucleic acid sequence or its complement. --

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-- 87. (NEW) The process of claim 86, wherein said providing step 1), at least one second initial primer or second nucleic acid construct is provided, wherein said second initial primer or second nucleic acid construct comprises a first segment substantially complementary to sequences that are synthesized after extension of said first initial primer or first nucleic acid construct. --

-- 88. (NEW) The process of claim 87, wherein said second initial primer or second nucleic acid construct further comprises a second segment being (i) substantially non-identical to the first segment of said second initial primer or nucleic acid construct; (ii) substantially identical to a portion of said extended first initial primer or nucleic acid construct; and (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said second initial primer or second nucleic acid construct with said extended first initial primer or first nucleic acid construct as a template. --

-- 89. (NEW) The process of claims 86, 87 or 88, wherein said first initial primers or constructs or said second initial primers or second nucleic acid constructs or both are converted into a form capable of stem-loop formation under isothermal conditions by the presence of the specific target nucleic acid sequence or its complement. --

-- 90. (NEW) The process of claims 86, 87 or 88, wherein said first initial primers or first nucleic acid constructs or said second initial primers or second nucleic acid constructs or both are converted into a form capable of stem-loop formation with one or more limited cycle or full cycle steps in the presence of the specific target nucleic acid sequence or its complement. --

-- 91. (NEW) The process of any of claims 86, 87, 88, 89 or 90, wherein less than about 50 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 92. (NEW) The process of claim 91, wherein less than about 10 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 93. (NEW) The process of any of claim 92, wherein the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct is adjacent to the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 94. (NEW) The process of claim 86, wherein said template polymerizing enzyme comprises a member selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, DNA ligase, and a combination of any of the foregoing. --

-- 95. (NEW) The process of claim 86, 87, 88, 89, 90, 91, 92, 93 or 94, wherein said first initial primers, extended first initial primers, first nucleic acid constructs or extended first nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 96. (NEW) The process of any of claims 86, 87, 88, 89, 90, 91, 92, 93 or 94, wherein any of said first initial primer or first nucleic acid constructs or said extended first initial primers or said extended first nucleic acid constructs or said second initial primers or said second nucleic acid constructs or said extended second initial primers or said extended second nucleic acid constructs comprise one or more modified nucleotides having detectable labels. --

-- 97. (NEW) The process of claims 95 or 96, wherein said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluoroscein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 98. (NEW) A process for detecting the presence of a specific target nucleic acid sequence comprising the steps of:

1) providing one or more first initial primers or first nucleic acid constructs comprising two segments:

(A) a first segment (i) being substantially complementary to a portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension, and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of the first initial primer or first nucleic acid construct with said specific target nucleic acid sequence as a template

2) mixing said first initial primer or first nucleic acid construct with substrates, buffer, a template-dependent polymerizing enzyme and a sample to be tested for the presence of said specific target nucleic acid

3) incubating said mixture under temperature conditions sufficient for binding of said initial primers or nucleic acid constructs to said specific target nucleic acid sequence, extension of said initial primers or nucleic acid constructs and formation of stem-loop structures; and

4) detecting the presence of said stem-loop structure formed by self-annealing between the second segment of said first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of said first initial primer or construct, thereby detecting the presence of said specific target nucleic acid sequence or its complement. --

-- 99. (NEW) The process of claim 98, wherein said providing step, a second initial primer or second nucleic acid construct is provided, wherein said second initial primer or second nucleic acid construct comprises a first segment substantially complementary to sequences that are synthesized after extension of said first initial primer or first nucleic acid construct. --

-- 100. (NEW) The process of claim 99, wherein said second initial primer or second nucleic acid construct further comprises a second segment being (i) substantially non-identical to the first segment of said second initial primer or second nucleic acid construct; (ii) substantially identical to a portion of said extended first initial primer or first nucleic acid construct; and (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said second initial primer or second nucleic acid construct with said extended first initial primer or nucleic acid construct as a template. --

-- 101. (NEW) The process of claims 98, 99 or 100, wherein first initial primers or first nucleic acid constructs or said second initial primers or second nucleic acid constructs or both are converted into a form capable of stem-loop formation under isothermal conditions by the presence of the specific target nucleic acid sequence or its complement. --

-- 102. (NEW) The process of claims 98, 99 or 100, wherein said first initial primers or first nucleic acid constructs or said second initial primers or second nucleic acid constructs or both are converted into a form capable of stem-loop formation with one or more limited cycle or full cycle steps in the presence of the specific target nucleic acid sequence or its complement. --

-- 103. (NEW) The process of claim 98, wherein said template polymerizing enzyme comprises a member selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, DNA ligase and a combination of any of the foregoing. --

-- 104. (NEW) The process of claim 98, 99, 100, 101, 102, or 103, wherein said first initial primers, extended first initial primers, first nucleic acid constructs or extended first nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 105. (NEW) The process of any of claims 98, 99, 100, 101, 102, 103 or 104, wherein any of said first initial primers or first nucleic acid constructs, said extended first initial primers or extended first nucleic acid constructs, said second initial primers or second nucleic acid constructs, or said second extended initial primers or extended second nucleic acid constructs comprise one or more modified nucleotides having detectable labels. --

-- 106. (NEW) The process of claims 104 or 105, wherein said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 107. (NEW) A process for amplifying a specific target nucleic acid sequence comprising the steps of:

1) providing:

- (i) said specific target nucleic acid sequence;
- (ii) one or more first initial primers or first nucleic acid constructs

comprising two segments:

(A) a first segment (i) being substantially complementary to a portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of the first initial primer or first nucleic acid construct with said specific target nucleic acid sequence as a template and wherein a stem-loop structure can be formed by self-annealing between the second segment of the first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of the first initial primer or first nucleic acid construct wherein the stability of a stem formed by such intrastrand hybridization is substantially equal to or is higher than the stability of a hybrid formed between said loop segment and its complement by interstrand hybridization;

2) mixing said first initial primers or nucleic acid constructs with substrates, buffer, a template-dependent polymerizing enzyme and a sample to be tested for the presence of said specific target nucleic acid; and

3) incubating said mixture under temperature conditions sufficient for binding of said first initial primers or first nucleic acid constructs to said specific target nucleic acid sequence, extension of said first initial primers or first nucleic acid constructs and formation of stem-loop structures, thereby producing one or more copies of said specific target nucleic acid sequence or its complement. --

-- 112. (NEW) The process of any of claims 107, 108, 109, 110 or 111, wherein less than about 50 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 113. (NEW) The process of claim 112, wherein less than about 10 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 114. (NEW) The process of claim 113, wherein the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct is adjacent to the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 115. (NEW) The process of claim 107, wherein said template polymerizing enzyme comprises a member selected from the group consisting of DNA polymerase, RNA polymerase, reverse transcriptase, DNA ligase and a combination of any of the foregoing. --

-- 116. (NEW) The process of claim 107, wherein said first initial primers, extended first initial primers, first nucleic acid constructs or extended first nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 117. (NEW) The process of claim 107, wherein said first initial primer or first nucleic acid construct or said extended first initial primer or first nucleic acid construct comprises one or more modified nucleotides having detectable labels. --

-- 118. (NEW) The process of claims 116 or 117, wherein said detectable labels are selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --



-- 119. (NEW) A process for detecting the presence of a specific target nucleic acid sequence comprising the steps of:

1) providing one or more first initial primers or first nucleic acid constructs comprising two segments:

(A) a first segment (i) being substantially complementary to a first portion of said specific target nucleic acid sequence and (ii) capable of template dependent-first extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that are synthesized by extension of the first segment of the first initial primer or first nucleic acid construct with said specific target nucleic acid sequence as a template and wherein a stem-loop structure can be created by self-annealing between the second segment of the first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of the first initial primer or first nucleic acid construct wherein the stability of a stem formed by such intrastrand hybridization is substantially equal to or is higher than the stability of a hybrid formed between said loop segment and its complement by interstrand hybridization;

2) mixing said first initial primer or first nucleic acid construct with substrates, buffer, a template-dependent polymerizing enzyme and a sample to be tested for the presence of said specific target nucleic acid;

3) incubating said mixture under temperature conditions sufficient for binding of said first initial primers or first nucleic acid constructs to said specific target nucleic acid sequence, extension of said first initial primers or first nucleic acid constructs and formation of stem-loop structures; and

4) detecting the presence of said stem-loop structure formed by self-annealing between the second segment of said first initial primer or first nucleic acid construct and a segment derived from target template dependent extension of the first segment of said first initial primer or first nucleic acid construct, thereby detecting the presence of said specific target nucleic acid sequence or its complement. --

-- 120. (NEW) The process of claim 119, wherein said providing step 1), a second initial primer or second nucleic acid construct is provided, wherein said second initial primer or second nucleic acid construct comprises a first segment substantially complementary to sequences that are synthesized after extension of said first initial primer or first nucleic acid construct. --

-- 121. (NEW) The process of claim 120, wherein said second initial primer or second nucleic acid construct further comprises a second segment being (i) substantially non-identical to the first segment of said second initial primer or second nucleic acid construct; (ii) substantially identical to a portion of said extended first initial primer or first nucleic acid construct; and (iii) substantially complementary to sequences that are synthesized by extension of the first segment of said second initial primer or second nucleic acid construct with said extended first initial primer or first nucleic acid construct as a template. --

-- 122. (NEW) The process of claims 119, 120 or 121, wherein the synthesis of one or more copies of sequences derived from the specific target nucleic acid sequence or its complement is carried out under isothermal conditions. --

-- 123. (NEW) The process of claims 119, 120 or 121, wherein the synthesis of one or more copies of sequences derived from the specific target nucleic acid sequence or its complement is carried out with one or more limited cycle or full cycle steps. --

-- 124. (NEW) The process of any of claims 120, 121, 122 or 123, wherein less than about 50 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 125. (NEW) The process of claim 124, wherein less than about 10 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 126. (NEW) The process of claim 125, wherein the portion of said specific target nucleic acid that is complementary to the first segment of the first initial primer or first nucleic acid construct is adjacent to the portion of said specific target nucleic acid that is identical to the second segment of the first initial primer or first nucleic acid construct. --

-- 127. (NEW) A composition comprising a primer or nucleic acid construct that is capable of producing one or more copies of a specific target nucleic acid sequence, wherein said primer or nucleic acid construct comprises at least two segments:

(A) a first segment (i) being substantially complementary to a first portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that can be synthesized by extension of the first segment of said primer or nucleic acid construct with said specific target nucleic acid sequence as a template and where in the absence of a denaturation step, said extended primer or said extended nucleic acid construct is capable of participation in the formation of a stem-loop structure after said specific target nucleic acid sequence is used as a template for extension. --

-- 128. (NEW) The process of claim 127, wherein said initial primers or nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 129. (NEW) The composition of claim 128, wherein said primer or nucleic acid construct or said extended primer or nucleic acid construct are capable of forming a stem-loop structure comprise one or more modified nucleotides having detectable labels. --

-- 130. (NEW) The composition of claims 128 or 129, where said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 131. (NEW) A composition comprising a primer or nucleic acid construct that is capable of producing one or more copies of a specific target nucleic acid sequence wherein said primer or nucleic acid construct comprises at least two segments:

(A) a first segment (i) being substantially complementary to a first portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that can be synthesized by extension of the first segment of said primer or nucleic acid construct with said specific target nucleic acid sequence as a template and wherein the portion of said specific target nucleic acid that comprises sequences complementary to the first segment of said primer or nucleic acid construct and the portion of said specific target nucleic acid that comprises sequences substantially identical to the second segment of said primer or nucleic acid construct are in close proximity to each other. --

-- 132. (NEW) The composition of claim 131, wherein less than about 50 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of said primer or nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of said primer or nucleic acid construct. --

-- 133. (NEW) The composition of claim 132, wherein less than about 10 nucleotides separate the portion of said specific target nucleic acid that is complementary to the first segment of said primer or nucleic acid construct from the portion of said specific target nucleic acid that is identical to the second segment of said primer or nucleic acid construct. --

-- 134. (NEW) The composition of claim 133, wherein the portion of said specific target nucleic acid that is complementary to the first segment of said primer or nucleic acid construct is adjacent to the portion of said specific target nucleic acid that is identical to the second segment of said primer or nucleic acid construct. --

-- 135. (NEW) The process of claim 132, 133 or 134, wherein said initial primer or nucleic acid construct comprises one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 136. (NEW) The composition of any of claims 131, 132, 133, 134 or 135, wherein said primer or nucleic acid construct comprises one or more modified nucleotides having detectable labels. --

-- 137. (NEW) The composition of claims 135 or 136, where said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

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-- 138. (NEW) A composition comprising a primer or nucleic acid construct that is capable of producing one or more copies of a specific target nucleic acid sequence wherein said primer or nucleic acid construct comprises at least two segments:

(A) a first segment (i) being substantially complementary to a first portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that can be synthesized by extension of the first segment of said primer or nucleic acid construct with said specific target nucleic acid sequence as a template and wherein a stem-loop structure can be created by self-annealing between the second segment of said primer or nucleic acid construct and a segment derived from target template dependent extension of the first segment of said primer or nucleic acid construct wherein the stability of a stem formed by such intrastrand hybridization is substantially equal to or is higher than the stability of a hybrid formed between said loop segment and its complement by interstrand hybridization. --

-- 139. (NEW) . The process of claim 138, wherein said initial primer or nucleic acid constructs comprise one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 140. (NEW) The composition of claim 139, wherein said primer or nucleic acid construct comprise one or more modified nucleotides having detectable labels. --

-- 141. (NEW) The composition of claims 139 or 140, where said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluoroscein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

-- 142. (NEW) A composition comprising a primer or nucleic acid construct that is capable of producing more than one copies of a specific target nucleic acid sequence wherein said primer or nucleic acid construct comprises at least two segments:

(A) a first segment (i) being substantially complementary to a first portion of said specific target nucleic acid sequence and (ii) capable of template dependent extension; and

(B) a second segment being (i) substantially non-identical to said first segment, (ii) substantially identical to a portion of said specific target nucleic acid sequence, (iii) substantially complementary to sequences that can be synthesized by extension of the first segment of said primer or nucleic acid construct with said specific target nucleic acid sequence as a template and iv) capable of providing for binding of a first segment of a second primer or nucleic acid construct to said first portion of said specific target nucleic acid sequence under isostatic or limited cycling conditions such that extension of said second primer or nucleic acid construct is capable of displacing said extended first primer or nucleic acid construct. --

-- 143. (NEW) The composition of claim 142, wherein said initial primer or nucleic acid construct comprises one or more moieties selected from the group consisting of modified nucleotides, non-nucleic acid polymers, branched nucleic acids, inverted nucleic acids, peptide nucleic acids, spacer groups, abasic sites, detectable labels and a combination of any of the foregoing. --

-- 144. (NEW) The composition of claims 142, wherein said primer or nucleic acid construct or said extended primer or nucleic acid construct comprises one or more modified nucleotides having detectable labels. --

-- 145. (NEW) The composition of claim 143 or 144, wherein said detectable labels comprise a member selected from the group consisting of haptens, ligands, receptors, fluorescein, rhodamine, coumarin, fluoresceinated molecules, infra-red fluorescent groups, chemiluminescent moieties, energy transfer systems, enzymes and a combination of any of the foregoing. --

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